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Roche-Neu.ST25.txt  
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&lt;110&gt; F. Hoffmann-La Roche AG

&lt;120&gt; IL-15 Antagonists

&lt;130&gt; Case21909

&lt;140&gt; PCT/CH03/00666

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&lt;160&gt; 30

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; human

&lt;400&gt; 1

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile  
1 5 10 15Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His  
20 25 30Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
35 40 45Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
50 55 60Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
65 70 75 80

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Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
                     85                                    90                                    95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn  
                     100                                    105                                    110

Thr Ser

<210> 2

<211> 231

<212> PRT

<213> human

<400> 2

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
   1                    5                                    10                                    15

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
                     20                                    25                                    30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
                     35                                    40                                    45

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
                     50                                    55                                    60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
   65                                    70                                    75                                    80

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
                     85                                    90                                    95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
                     100                                    105                                    110

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
                     115                                    120                                    125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys  
                     130                                    135                                    140

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
   145                                    150                                    155                                    160

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
                     165                                    170                                    175

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Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 180 185 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 195 200 205

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 210 215 220

Leu Ser Leu Ser Pro Gly Lys  
 225 230

<210> 3

<211> 232

<212> PRT

<213> mouse

<400> 3

Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala  
 1 5 10 15

Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile  
 20 25 30

Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val  
 35 40 45

Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val  
 50 55 60

Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp  
 65 70 75 80

Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln  
 85 90 95

Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp  
 100 105 110

Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val  
 115 120 125

Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr  
 130 135 140

Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu  
 145 150 155 160

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Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr  
 165 170 175

Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr  
 180 185 190

Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr  
 195 200 205

Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys  
 210 215 220

Ser Phe Ser Arg Thr Pro Gly Lys  
 225 230

&lt;210&gt; 4

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; fusion protein

&lt;400&gt; 4

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Thr Glu Asp Leu Ile  
 1 5 10 15

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His  
 20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
 35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
 50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
 65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
 85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn  
 100 105 110

Thr Ser Asp Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys  
 115 120 125

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 130 135 140  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 145 150 155 160  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
 165 170 175  
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 180 185 190  
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
 195 200 205  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 210 215 220  
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
 225 230 235 240  
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
 245 250 255  
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 260 265 270  
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 275 280 285  
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 290 295 300  
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
 305 310 315 320  
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
 325 330 335  
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 340 345

&lt;210&gt; 5

&lt;211&gt; 347

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

Roche-Neu.ST25.txt

&lt;223&gt; fusion protein

&lt;400&gt; 5

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Thr Glu Asp Leu Ile  
1 5 10 15

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His  
20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn  
100 105 110

Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys  
115 120 125

Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro  
130 135 140

Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr  
145 150 155 160

Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser  
165 170 175

Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His  
180 185 190

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile  
195 200 205

Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn  
210 215 220

Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys  
225 230 235 240

Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu  
245 250 255

Roche-Neu.ST25.txt

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe  
                   260                                  265                                  270

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu  
                   275                                  280                                  285

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr  
                   290                                  295                                  300

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg  
                   305                                  310                                  315                                  320

Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His  
                                   325                                  330                                  335

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
                   340                                  345

&lt;210&gt; 6

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 6

aactgggtga atgtaataag tgatttgaaa aaaattgaag atcttattca atctatgcat 60  
 attgatgcta ctttatatac ggaaagtgat gttcacccca gttgcaaagt aacagcaatg 120  
 aagtgccttc tcttgaggtt acaagttatt tcacttgagt ccggagatgc aagtattcat 180  
 gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tgggaatgta 240  
 acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg 300  
 cagagttttg tacatattgt ccaaattgtc atcaacactt c 341

&lt;210&gt; 7

&lt;211&gt; 697

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 7

cccaaatctg ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 60  
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccgacc 120  
 cctgagggtca cgtgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 180  
 tgggtacgtg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 240  
 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 300

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 360  
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat 420  
gagctgacca agaaccaggt cagcctgacc tgcttgggtca aaggcttcta tcccagcgac 480  
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 540  
gtgctggact ccgacggctc cttcttcttc tacagcaagc tcaccgtgga caagagcagg 600  
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggtcttgca caaccactac 660  
acgcagaaga gcctctccct gtctccgggt aaatgat 697

<210> 8

<211> 700

<212> DNA

<213> mouse

<400> 8  
cccagagggc ccacaatcaa gccctgtcct ccatgcaaat gcccagcacc taacctcttg 60  
ggtggaccat ccgtcttcat cttccctcca aagatcaagg atgtactcat gatctccctg 120  
agcccatag tcacatgtgt ggtggtggat gtgagcgagg atgaccaga tgtccagatc 180  
agctggtttg tgaacaacgt ggaagtacac acagctcaga cacaaacca tagagaggat 240  
tacaacagta ctctccgggt ggtcagtgcc ctcccatcc agcaccagga ctggatgagt 300  
ggcaaggagt tcaaatgcaa ggtcaacaac aaagacctcc cagcgcccat cgagagaacc 360  
atctcaaac ccaaagggtc agtaagagct ccacaggat atgtcttgcc tccaccagaa 420  
gaagagatga ctaagaaaca ggtcactctg acctgcatgg tcacagactt catgcctgaa 480  
gacatttacg tggagtggac caacaacggg aaaacagagc taaactacaa gaacactgaa 540  
ccagtcttgg actctgatgg ttcttacttc atgtacagca agctgagagt ggaaaagaag 600  
aactgggtgg aaagaaatag ctactcctgt tcagtggctc acgaggggtc gcacaatcac 660  
cacacgacta agagcttctc ccggactccg ggtaaatgag 700

<210> 9

<211> 1047

<212> DNA

<213> artificial sequence

<220>

<223> DNA coding for fusion protein

<400> 9  
aactgggtga atgtaataag tgatttgaaa aaaaccgaag atcttattca atctatgcat 60



## Roche-Neu.ST25.txt

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attgatgcta ctttatatac ggaaagtgat gttcacccca gttgcaaagt aacagcaatg 120
aagtgccttc tcttgaggtt acaagttatt tcacttgagt ccggagatgc aagtattcat 180
gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tgggaatgta 240
acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg 300
cagagttttg tacatattgt ccaaagtgtc atcaacactt cggatcccaa atctgctgac 360
aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagtcttc 420
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacgtgc 480
gtggtggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 540
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 600
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 660
aaggtctcca acaagaccct ccagccccc atcgagaaaa ccatctccaa agccaaaggg 720
cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac 780
caggtcagcc tgacctgcct ggtcaaaggc ttctatcca gcgacatcg cgtggagtgg 840
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 900
ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggc gcaggggaac 960
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1020
tcctgtctc cgggtaaatg atctaga 1047

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&lt;210&gt; 10

&lt;211&gt; 1045

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; DNA for fusion protein

&lt;400&gt; 10

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aactgggtga atgtaataag tgatttgaaa aaaattgaag atcttattca atctatgcat 60
attgatgcta ctttatatac ggaaagtgat gttcacccca gttgcaaagt aacagcaatg 120
aagtgccttc tcttgaggtt acaagttatt tcacttgagt ccggagatgc aagtattcat 180
gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tgggaatgta 240
acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg 300
cagagttttg tacatattgt ccaaagtgtc atcaacactt cggatcccag agggcccaca 360
atcaagccct gtcctccatg caaatgccc gcacctaacc tcttggtggtg accatccgtc 420
ttcatcttcc ctcaaagat caaggatgta ctcatgatct ccctgagccc catagtcaca 480
tgtgtggtg tggatgtgag cgaggatgac ccagatgtcc agatcagctg gtttgtgaac 540

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## Roche-Neu.ST25.txt

aacgtggaag tacacacagc tcagacacaa acccatagag aggattacaa cagtactctc 600  
cgggtggtca gtgccctccc catccagcac caggactgga tgagtggcaa ggagttcaaa 660  
tgcaagggtca acaacaaaga cctcccagcg cccatcgaga gaaccatctc aaaacccaaa 720  
gggtcagtaa gagctccaca ggtatatgtc ttgcctccac cagaagaaga gatgactaag 780  
aaacagggtca ctctgacctg catggtcaca gacttcatgc ctgaagacat ttacgtggag 840  
tggaccaaca acgggaaaac agagctaaac tacaagaaca ctgaaccagt cctggactct 900  
gatggttctt acttcatgta cagcaagctg agagtggaaa agaagaactg ggtggaaaga 960  
aatagctact cctgttcagt ggtccacgag ggtctgcaca atcaccacac gactaagagc 1020  
ttctcccgga ctccgggtaa atgag 1045

<210> 11  
<211> 63  
<212> DNA  
<213> human

<400> 11  
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gac 63

<210> 12  
<211> 72  
<212> DNA  
<213> human

<400> 12  
atgcccattg ggtctctgca accgctggcc accttgatgac tgctggggat gctggctgct 60  
tcctgcctcg ga 72

<210> 13  
<211> 75  
<212> DNA  
<213> human

<400> 13  
atgaaccggg gagtcccttt taggcacttg cttctggtgc tgcaactggc gctcctccca 60  
gcagccactc agga 75

Roche-Neu.ST25.txt

&lt;210&gt; 14

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 14

atgtacagga tgcaactcct gtcttgcatc gcactaagtc ttgcacttgt cacaaacagt 60

&lt;210&gt; 15

&lt;211&gt; 68

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 15

tgaaagtctc tgccgccctt ctgtgcctgc tgctcatagc agccaccttc attccccaag 60  
ggctcgct 68

&lt;210&gt; 16

&lt;211&gt; 40

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 16

atgtcttcat tttgggctgt ttcagtcag ggcttcctaa 40

&lt;210&gt; 17

&lt;211&gt; 144

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 17

atgagaattt cgaaaccaca tttgagaagt atttccatcc agtgctactt gtgtttactt 60  
ctaaacagtc attttctaac tgaagctggc attcatgtct tcattttggg ctgtttcagt 120  
gcaggggcttc ctaaaacaga agcc 144

&lt;210&gt; 18

&lt;211&gt; 74

&lt;212&gt; DNA

Roche-Neu.ST25.txt

<213> artificial sequence

<220>

<223> oligonucleotide

<400> 18  
ctagccacca tggagacaga cacactcctg ctatgggtac tgctgctctg ggttcagggt 60  
tccactggtg acaa 74

<210> 19

<211> 74

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide

<400> 19  
ccagttgtca ccagtggaac ctggaacca gaggcagcagt acccatagca ggagtgtgtc 60  
tgtctccatg gtgg 74

<210> 20

<211> 36

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide

<400> 20  
ctgggtgaat gtaataagtg atttgaaaaa aattga 36

<210> 21

<211> 37

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide

<400> 21  
gatcttcaat ttttttcaaa tcacttatta cattcac 37

Roche-Neu.ST25.txt

&lt;210&gt; 22

&lt;211&gt; 111

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide

&lt;400&gt; 22

ctagccacca tggagacaga cacactcctg ctatgggtac tgctgctctg ggttccaggt 60  
 tccactgggtg acaactgggt gaatgtaata agtgatttga aaaaaattga a 111

&lt;210&gt; 23

&lt;211&gt; 111

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide

&lt;400&gt; 23

ggtggtacct ctgtctgtgt gaggagcata cccatgacga cgagacccaa ggtccaaggt 60  
 gaccactgaa gaccactta cattattcac taaacttttt ttaacttcta g 111

&lt;210&gt; 24

&lt;211&gt; 347

&lt;212&gt; PRT

&lt;213&gt; human

&lt;400&gt; 24

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile  
 1 5 10 15

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His  
 20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
 35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
 50 55 60

Roche-Neu.ST25.txt

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
 65 70 75 80  
 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
 85 90 95  
 Lys Glu Phe Leu Asp Ser Phe Val His Ile Val Asp Met Phe Ile Asn  
 100 105 110  
 Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys  
 115 120 125  
 Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro  
 130 135 140  
 Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr  
 145 150 155 160  
 Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser  
 165 170 175  
 Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His  
 180 185 190  
 Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile  
 195 200 205  
 Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn  
 210 215 220  
 Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys  
 225 230 235 240  
 Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu  
 245 250 255  
 Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe  
 260 265 270  
 Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu  
 275 280 285  
 Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr  
 290 295 300  
 Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg  
 305 310 315 320  
 Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His  
 325 330 335

Roche-Neu.ST25.txt

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
                   340                                  345

&lt;210&gt; 25

&lt;211&gt; 347

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; mutated Fc

&lt;400&gt; 25

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile  
   1                  5                                  10                                  15

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His  
                   20                                  25                                  30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
                   35                                  40                                  45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
   50                                  55                                  60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
   65                                  70                                  75                                  80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
                   85                                  90                                  95

Lys Glu Phe Leu Asp Ser Phe Val His Ile Val Gln Met Phe Ile Asn  
                   100                                  105                                  110

Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys  
                   115                                  120                                  125

Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro  
   130                                  135                                  140

Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr  
   145                                  150                                  155                                  160

Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser  
                   165                                  170                                  175

Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His  
                   180                                  185                                  190

Roche-Neu.ST25.txt

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile  
 195 200 205  
 Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn  
 210 215 220  
 Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys  
 225 230 235 240  
 Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu  
 245 250 255  
 Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe  
 260 265 270  
 Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu  
 275 280 285  
 Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr  
 290 295 300  
 Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg  
 305 310 315 320  
 Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His  
 325 330 335  
 Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
 340 345

&lt;210&gt; 26

&lt;211&gt; 1108

&lt;212&gt; DNA

&lt;213&gt; human

<400> 26  
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 gacaactggg tgaatgtaat aagtgatttg aaaaaaattg aagatcttat tcaatctatg 120  
 catattgatg ctactttata tacggaaagt gatgttcacc ccagttgcaa agtaacagca 180  
 atgaagtgct ttctcttgga gttacaagtt atttcacttg agtccggaga tgcaagtatt 240  
 catgatacag tagaaaatct gatcatccta gcaacaaca gtttgtcttc taatgggaat 300  
 gtaacagaat ctggatgcaa agaattgtgag gaactggagg aaaaaaatat taaagaattt 360  
 ttggacagtt ttgtacatat tgctgacatg ttcacaaaca cttcggatcc cagagggccc 420  
 acaatcaagc cctgtcctcc atgcaaatgc ccagcaccta acctcttggg tggaccatcc 480



Roche-Neu.ST25.txt

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acatgtgtgg tgggtggatgt gagcgaggat gaccagatg tccagatcag ctggtttgtg      600
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gagtggacca acaacgggaa aacagagcta aactacaaga aactgaacc agtcctggac      960
tctgatggtt cttacttcat gtacagcaag ctgagagtgg aaaagaagaa ctgggtggaa     1020
agaaatagct actcctgttc agtggccac gagggctcgc acaatcacca cacgactaac     1080
agcttctccc ggactccggg taaatgag                                     1108

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&lt;210&gt; 27

&lt;211&gt; 1108

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; nucleic acid for mutated Fc

&lt;400&gt; 27

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gacaactggg tgaatgtaat aagtgatttg aaaaaattg aagatcttat tcaatctatg     120
catattgatg ctactttata tacggaaagt gatgttcacc ccagttgcaa agtaacagca     180
atgaagtgct ttctcttga gttacaagtt atttcacttg agtccggaga tgcaagtatt     240
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acaatcaagc cctgtcctcc atgcaaatgc ccagcaccta acctcttggg tggaccatcc     480
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Roche-Neu.ST25.txt

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agaaatagct actcctgttc agtgggtccac gaggggtctgc acaatcacca cacgactaag 1080  
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&lt;210&gt; 28

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 28

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&lt;210&gt; 29

&lt;211&gt; 56

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 29

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&lt;210&gt; 30

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 30

gggatccgaa gtgttgatga acatttggga 29